

RAW SEQUENCE LISTING

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Application Serial Number: 10/552,061
Source: Pg 7/10
Date Processed by STIC: 10/17/05

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PCT

RAW SEQUENCE LISTING

DATE: 10/17/2005

PATENT APPLICATION: US/10/552,061

TIME: 10:57:43

Input Set : A:\5.1277.1.txt

Output Set: N:\CRF4\10172005\J552061.raw

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3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
5 <120> TITLE OF INVENTION: Nerve Regenerating Drug
7 <130> FILE REFERENCE: 5.1277
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/552,061
C--> 10 <141> CURRENT FILING DATE: 2005-10-04
12 <150> PRIOR APPLICATION NUMBER: PCT/JP04/005503
13 <151> PRIOR FILING DATE: 2004-04-16
15 <150> PRIOR APPLICATION NUMBER: JP2003-114579
16 <151> PRIOR FILING DATE: 2003-04-18
18 <160> NUMBER OF SEQ ID NOS: 17
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 420
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
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34 Asp Gly Ser Lys Val Thr Thr Val Val Ala Thr Pro Gly Gln Gly Pro
35   35               40               45
37 Asp Arg Pro Gln Glu Val Ser Tyr Thr Asp Thr Lys Val Ile Gly Asn
38   50               55               60
40 Gly Ser Phe Gly Val Val Tyr Gln Ala Lys Leu Cys Asp Ser Gly Glu
41  65               70               75               80
43 Leu Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg
44               85               90               95
46 Glu Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu
47   100             105             110
49 Arg Tyr Phe Phe Tyr Ser Ser Gly Glu Lys Lys Asp Glu Val Tyr Leu
50   115             120             125
52 Asn Leu Val Leu Asp Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg
53   130             135             140
55 His Tyr Ser Arg Ala Lys Gln Thr Leu Pro Val Ile Tyr Val Lys Leu
56 145             150             155             160
58 Tyr Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Phe Gly
59   165             170             175
61 Ile Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Asp
62   180             185             190
64 Thr Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val
65   195             200             205
67 Arg Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala

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68      210      215      220
70 Pro Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val
71 225      230      235      240
73 Trp Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Ile
74      245      250      255
76 Phe Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val
77      260      265      270
79 Leu Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr
80      275      280      285
82 Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Val
83      290      295      300
85 Phe Arg Pro Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Arg Leu
86 305      310      315      320
88 Leu Glu Tyr Thr Pro Thr Ala Arg Leu Thr Pro Leu Glu Ala Cys Ala
89      325      330      335
91 His Ser Phe Phe Asp Glu Leu Arg Asp Pro Asn Val Lys His Pro Asn
92      340      345      350
94 Gly Arg Asp Thr Pro Ala Leu Phe Asn Phe Thr Thr Gln Glu Leu Ser
95      355      360      365
97 Ser Asn Pro Pro Leu Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile
98      370      375      380
100 Gln Ala Ala Ala Ser Thr Pro Thr Asn Ala Thr Ala Ala Ser Asp Ala
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112 <213> ORGANISM: Homo sapiens
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119 gtg cag cag cct tca gct ttt ggc agc atg aaa gtt agc aga gac aag 96
120 Val Gln Gln Pro Ser Ala Phe Gly Ser Met Lys Val Ser Arg Asp Lys
121 20 25 30
123 gac ggc agc aag gtg aca aca gtg gtg gca act cct ggg cag ggt cca 144
124 Asp Gly Ser Lys Val Thr Thr Val Val Ala Thr Pro Gly Gln Gly Pro
125 35 40 45
127 gac agg cca caa gaa gtc agc tat aca gac act aaa gtg att gga aat 192
128 Asp Arg Pro Gln Glu Val Ser Tyr Thr Asp Thr Lys Val Ile Gly Asn
129 50 55 60
131 gga tca ttt ggt gtg gta tat caa gcc aaa ctt tgt gat tca gga gaa 240
132 Gly Ser Phe Gly Val Val Tyr Gln Ala Lys Leu Cys Asp Ser Gly Glu
133 65 70 75 80
135 ctg gtc gcc atc aag aaa gta ttg cag gac aag aga ttt aag aat cga 288
136 Leu Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg

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140	Glu Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu							
141		100		105		110		
143	cgt tat ttc ttc tac tcc agt ggt gag aag aaa gat gag gtc tat ctt							384
144	Arg Tyr Phe Phe Tyr Ser Ser Gly Glu Lys Lys Asp Glu Val Tyr Leu							
145		115		120		125		
147	aat ctg gtg ctg gac tat gtt ccg gaa aca gta tac aga gtt gcc aga							432
148	Asn Leu Val Leu Asp Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg							
149		130		135		140		
151	cac tat agt cga gcc aaa cag acg ctc cct gtg att tat gtc aag ttg							480
152	His Tyr Ser Arg Ala Lys Gln Thr Leu Pro Val Ile Tyr Val Lys Leu							
153	145		150		155		160	
155	tat atg tat cag ctg ttc cga agt tta gcc tat atc cat tcc ttt gga							528
156	Tyr Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Phe Gly							
157		165		170		175		
159	atc tgc cat cgg gat att aaa ccg cag aac ctc ttg ttg gat cct gat							576
160	Ile Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Asp							
161		180		185		190		
163	act gct gta tta aaa ctc tgt gac ttt gga agt gca aag cag ctg gtc							624
164	Thr Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val							
165		195		200		205		
167	cga gga gaa ccc aat gtt tcg tat atc tgt tct cgg tac tat agg gca							672
168	Arg Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala							
169		210		215		220		
171	cca gag ttg atc ttt gga gcc act gat tat acc tct agt ata gat gta							720
172	Pro Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val							
173	225		230		235		240	
175	tgg tct gct ggc tgt gtg ttg gct gag ctg tta cta gga caa cca ata							768
176	Trp Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Gly Gln Pro Ile							
177		245		250		255		
179	ttt cca ggg gat agt ggt gtg gat cag ttg gta gaa ata atc aag gtc							816
180	Phe Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val							
181		260		265		270		
183	ctg gga act cca aca agg gag caa atc aga gaa atg aac cca aac tac							864
184	Leu Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr							
185		275		280		285		
187	aca gaa ttt aaa ttc cct caa att aag gca cat cct tgg act aag gtc							912
188	Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Val							
189		290		295		300		
191	ttc cga ccc cga act cca ccg gag gca att gca ctg tgt agc cgt ctg							960
192	Phe Arg Pro Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Arg Leu							
193	305		310		315		320	
195	ctg gag tat aca cca act gcc cga cta aca cca ctg gaa gct tgt gca							1008
196	Leu Glu Tyr Thr Pro Thr Ala Arg Leu Thr Pro Leu Glu Ala Cys Ala							
197		325		330		335		
199	cat tca ttt ttt gat gaa tta cgg gac cca aat gtc aaa cat cca aat							1056
200	His Ser Phe Phe Asp Glu Leu Arg Asp Pro Asn Val Lys His Pro Asn							
201		340		345		350		

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203 ggg cga gac aca cct gca ctc ttc aac ttc acc act caa gaa ctg tca 1104
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205      355      360      365
207 agt aat cca cct ctg gct acc atc ctt att cct cct cat gct cgg att 1152
208 Ser Asn Pro Pro Leu Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile
209      370      375      380
211 caa gca gct gct tca acc ccc aca aat gcc aca gca gcg tca gat gct 1200
212 Gln Ala Ala Ala Ser Thr Pro Thr Asn Ala Thr Ala Ala Ser Asp Ala
213 385      390      395      400
215 aat act gga gac cgt gga cag acc aat aat gct gct tct gca tca gct 1248
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225 <212> TYPE: PRT
226 <213> ORGANISM: Homo sapiens
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233      20      25      30
235 Ala Trp Glu Val Ala Asn Lys Val Gly Gly Ile Tyr Thr Val Leu Gln
236      35      40      45
238 Thr Lys Ala Lys Val Thr Gly Asp Glu Trp Gly Asp Asn Tyr Phe Leu
239      50      55      60
241 Val Gly Pro Tyr Thr Glu Gln Gly Val Arg Thr Gln Val Glu Leu Leu
242 65      70      75      80
244 Glu Ala Pro Thr Pro Ala Leu Lys Arg Thr Leu Asp Ser Met Asn Ser
245      85      90      95
247 Lys Gly Cys Lys Val Tyr Phe Gly Arg Trp Leu Ile Glu Gly Gly Pro
248      100      105      110
250 Leu Val Val Leu Leu Asp Val Gly Ala Ser Ala Trp Ala Leu Glu Arg
251      115      120      125
253 Trp Lys Gly Glu Leu Trp Asp Ile Cys Asn Ile Gly Val Pro Trp Tyr
254      130      135      140
256 Asp Arg Glu Ala Asn Asp Ala Val Leu Phe Gly Phe Leu Thr Thr Trp
257 145      150      155      160
259 Phe Leu Gly Glu Phe Leu Ala Gln Ser Glu Glu Lys Pro His Val Val
260      165      170      175
262 Ala His Phe His Glu Trp Leu Ala Gly Val Gly Leu Cys Leu Cys Arg
263      180      185      190
265 Ala Arg Arg Leu Pro Val Ala Thr Ile Phe Thr Thr His Ala Thr Leu
266      195      200      205
268 Leu Gly Arg Tyr Leu Cys Ala Gly Ala Val Asp Phe Tyr Asn Asn Leu
269      210      215      220
271 Glu Asn Phe Asn Val Asp Lys Glu Ala Gly Glu Arg Gln Ile Tyr His

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272 225          230          235          240
274 Arg Tyr Cys Met Glu Arg Ala Ala Ala His Cys Ala His Val Phe Thr
275          245          250          255
277 Thr Val Ser Gln Ile Thr Ala Ile Glu Ala Gln His Leu Leu Lys Arg
278          260          265          270
280 Lys Pro Asp Ile Val Thr Pro Asn Gly Leu Asn Val Lys Lys Phe Ser
281          275          280          285
283 Ala Met His Glu Phe Gln Asn Leu His Ala Gln Ser Lys Ala Arg Ile
284          290          295          300
286 Gln Glu Phe Val Arg Gly His Phe Tyr Gly His Leu Asp Phe Asn Leu
287 305          310          315          320
289 Asp Lys Thr Leu Tyr Phe Phe Ile Ala Gly Arg Tyr Glu Phe Ser Asn
290          325          330          335
292 Lys Gly Ala Asp Val Phe Leu Glu Ala Leu Ala Arg Leu Asn Tyr Leu
293          340          345          350
295 Leu Arg Val Asn Gly Ser Glu Gln Thr Val Val Ala Phe Phe Ile Met
296          355          360          365
298 Pro Ala Arg Thr Asn Asn Phe Asn Val Glu Thr Leu Lys Gly Gln Ala
299          370          375          380
301 Val Arg Lys Gln Leu Trp Asp Thr Ala Asn Thr Val Lys Glu Lys Phe
302 385          390          395          400
304 Gly Arg Lys Leu Tyr Glu Ser Leu Leu Val Gly Ser Leu Pro Asp Met
305          405          410          415
307 Asn Lys Met Leu Asp Lys Glu Asp Phe Thr Met Met Lys Arg Ala Ile
308          420          425          430
310 Phe Ala Thr Gln Arg Gln Ser Phe Pro Pro Val Cys Thr His Asn Met
311          435          440          445
313 Leu Asp Asp Ser Ser Asp Pro Ile Leu Thr Thr Ile Arg Arg Ile Gly
314          450          455          460
316 Leu Phe Asn Ser Ser Ala Asp Arg Val Lys Val Ile Phe His Pro Glu
317 465          470          475          480
319 Phe Leu Ser Ser Thr Ser Pro Leu Leu Pro Val Asp Tyr Glu Glu Phe
320          485          490          495
322 Val Arg Gly Cys His Leu Gly Val Phe Pro Ser Tyr Tyr Glu Pro Trp
323          500          505          510
325 Gly Tyr Thr Pro Ala Glu Cys Thr Val Met Gly Ile Pro Ser Ile Ser
326          515          520          525
328 Thr Asn Leu Ser Gly Phe Gly Cys Phe Met Glu Glu His Ile Ala Asp
329          530          535          540
331 Pro Ser Ala Tyr Gly Ile Tyr Ile Leu Asp Arg Arg Phe Arg Ser Leu
332 545          550          555          560
334 Asp Asp Ser Cys Ser Gln Leu Thr Ser Phe Leu Tyr Ser Phe Cys Gln
335          565          570          575
337 Gln Ser Arg Arg Gln Arg Ile Ile Gln Arg Asn Arg Thr Glu Arg Leu
338          580          585          590
340 Ser Asp Leu Leu Asp Trp Lys Tyr Leu Gly Arg Tyr Tyr Met Ser Ala
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343 Arg His Met Ala Leu Ser Lys Ala Phe Pro Glu His Phe Thr Tyr Glu
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/552,061

DATE: 10/17/2005

TIME: 10:57:44

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Output Set: N:\CRF4\10172005\J552061.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date